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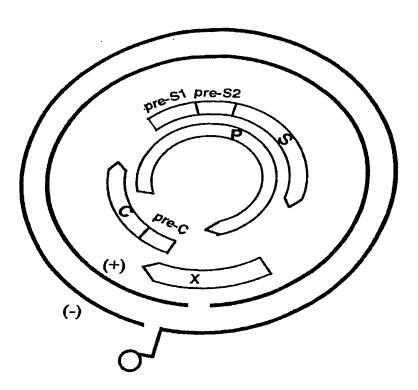


Figure 1

Figure 2

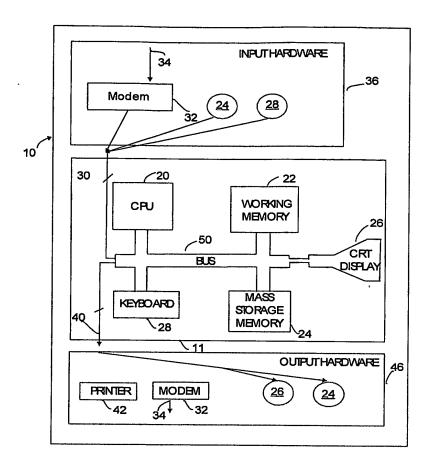


Figure 3A

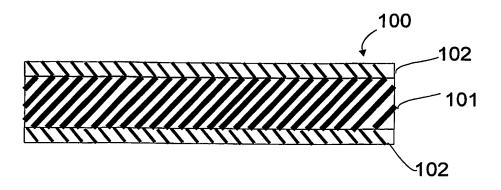


Figure 3B

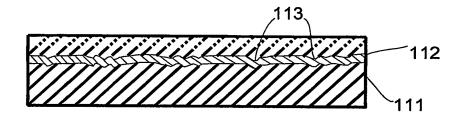


Figure 3C

Figure	4:	Patient	A n	t sequence			
			1	0 20	30	40	50
		GCTTC	CACC	AATCGGCAGGC	AGGAAGACAG	CCTACTCCCA:	CTCTCCACC
			6	70	80	90	100
		TCTAAC	_	CAGTCATCCTC	AGGCCATGCA	₽₽ ₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	100 AGCACATTCC
							IOCHCHIICC
			110			140	150
		ACCATO	CTC	rgctagatccc	AGACCTGCTG	STGGCTCCAG	TTCCGGAACA
			160	170	100		
		GTAAAC	160 CCTC		180	190	200
		OIMMC	CCI	GTTCCGACTAC	TGCCTCTCCC	ATATEGTEAAT	CTTCTCGAG
			. 210	220	230	240	250
		GACTGG	GGA	CCTGCGCCGA	ATATGGAGAGC	CACCACATCAG	250 GATTCCTAG
			260	270	280	290	300
		GACCCC	TGCI	CGTGTTACAG	GCGGGGTTTTI	CTTGTTGACA	AGAATCCTC
			310	320	330	0.10	
		АСААТА		AGAGTCTAGA(340	350
			.00111	INDITION OF THE PROPERTY OF TH	CICGIGGIGGE	CTTCTCTCAA	TTTTCTAGG
			360	370	380	390	400
		GGGAGC	ACCC	ACGTGTCCTG			CCTCCAATC
		3.0000	410	420	430	440	450
		ACTCAC	CAAC	CTCTTGTCCTC	CCAATTTGTCC	TGGTTATCGC	TGGATGTGT
			460	470	480	400	
		CTGCGG	-	TTATCATCTTC	⁴ᢐ∪ ℃ᡢᡢᡊᡢᡊᡊᡊ	490 TCCTCCTATC	500
					CICITORICO	IGCIGCIAIG	CCTCATCTT
			510	520	530	540	550
		CTTGTT	GGTT	CTTCTGGACT	ACCAAGGTATG	TTGCCCGTTT	GTCCTCTAC
		mmcan c		570	580	590	600
		TTCCAG	GAAC	ATCAACTACCA	AGCACGGGACC.	ATGCAAGACC	TGCACGACT
			610	620	630	640	650
		CCTGCT		GAACCTCTATG			650
						OTTOCTOTAC	AAAACCIIC
			660	670	680	690	700
		GGACGG	TAAP	TGCACTTGTAT	TCCCATCCCA	TCATCTTGGG	CTTTCGTAA
			= - 0				
	-	CATTOCCO	710	720	730	740	75_0
		GATTCCT	LATG	GGAGTGGGCCT	CAGTCCGTTT	CTCCTGGTTC	AGTTTACTA
			760	770	780	790	000
		GTGCCAT		,,, TCAGTGGTTC			008 יייהפכריייייתר
						JOCOLAUTUI.	TOGCTITC
			810	820	830	840	850

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AGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCTTGA

860 870 880 890 900

ATCCCTTTATACCGCTATTACCAATTTTCTTTTGTCTTTGGGTATACATT

910 920 930 940 950

TAAACCCTAATAAAACCAAGCGTTGGGGCTACTCCCTTAACTTCATGGGA

960 970 980 990 1000

TATGTAATTGGAAGTTGGGGTACCTTGCCACAGGAACATATTGTACAAAA

AATCAAA

Figure	5:	Patient	Α.	HBV	Polymerase	sequence
--------	----	---------	----	-----	------------	----------

-	LO YGEHHIRIPI	20 RTPARVTGGV	30 FLVDKNPHNT	40 KESRLVVDFS	50 QFS
_	50 PKFAVPNLQS	70 SLTNLLSSNL	80 SWLSLDVSAA	90 FYHLPLHPAA	100 MPH
11 LLVGSSGLF			130 TMQDLHDSCS:		150 YKT
16 FGRKLHLYS			180 FLLVQFTSAI		200 CLA
21 FSYMDDVVL	_		230 LLSLGIHLNPI		250 NFM
26 GYVIGSWGT		270 KIK			

Figure 5

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Figure 6: Patient A HBV HbsAg sequence

MESTTSGFLGPLLVLQAGFFLLTRILTIPKSLDSWWTSLNFLGGAPTCPG QNLQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLCLIFLLVLLDY QGMLPVCPLLPGTSTTSTGPCKTCTTPAQGTSMFPSCCCTKPSDGNCTCI PIPSSWAFVRFLWEWASVRFSWFSLLVPFVQWFVGLSPTVWLSVIWMMWY 210 220 WGPSLYNILNPFIPLLPIFFCLWVYI

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Figure 7: Patient B HBV NT sequence

10 TCTGTCTCCACCT	20 TTGAGAGACAC	30 TCATCCTCA	40 GGCCATGCAG	50 GGAACT
60 CCACAACCTTCCA	70 CCAAACTCTGO	80 CAAGATCCCA	90 GAGTGAGAGG	100 CCTGTAT
	120	130	140	150
160	170	180	190	200
TGTCTCTCACACA	TCGTCAATCTT	'CTCGAGGAT	TGGGGTCCCT	SCGCTGA
210 ACATGGAGAACAT	220 CACATCAGGAT			
260 GCGGGGTTTTTCT	270 TGTTGACAAGA			
310 CTCGTGGTGGACT			340 AACTACCGTG1	
360 GCCAAAATTCGCA			390 CACCAACCTCO	
	420	430	440	450
460	470	480	490	500
CCTCTTCATCCTG				
510 ATCAAGGTATGTT		530 CTCTAATTC		
560 AGCACGGGACCAT		580 ACGACTCCT		
610 GTATCCCTCCTGT	620 IGCTGTACCAA			
660 TTCCCATCCCATC	670 ATCCTGGGCTT			
710 TCAGCCCGTTTCT				

Figure 7

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76	50	770	780	790	800
CGTAGGGCT	TTCCCCCA	CTGTTTGGCT	TTCAGTTATA	ATGGATGATGT	GGT
0.1		000	000	0.40	0-0
81	LO	820	830	840	850
ATTGGGGG	CCAAGTCT	TATCGCATCI	TGAGTCCCTT	TTTACCGCTG	TTA
86	50	870	880	000	000
= '		•		890	900
CCAATTTTC	CTTTTGTCI	TTGGGTATAC	CATTTAAACCC	CTCACAAAACA	AAA
91	۱.0	920	930	940	950
AGATGGGGT	CACTCTTI	ACATTTCATO	GGCTATGTC <i>I</i>	ATTGGATGTTA	TGG
96	50	970	980		
_					
GICHTIGC	CACAAGATC	CACATCAGACA	GAAAA		

Figure 7 continued

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Figure	8:	Patient	В	POLYMERASE	sequence
--------	----	---------	---	------------	----------

EDWGPCAE	10	20	30	40	50
	EHGEHHIRI	PRTPARVTGGV	FLVDKNPHNI	FAESRLVVDFS	SQFS
RGNYRVSW	60	70	80	90	100
	VPKFAVPNLO	QSLTNLLSSNI	SWLSLDVSA	AFYHLPLHPAA	MPH
· -	.10	120	130	140	150
	LSRYVARLS	SNSRIFNHQHG	TMQNLHDSCS	SRKLYVSLLLI	YQT
_	.60	170	180	190	200
	SHPIILGFI	RKIPMGVGLSP	FLLAQFTSAI	CSVVRRAFPH	CLA
·	210	220	230	240	250
	/LGAKSVSHI	SESLFTAVTNF	LLSLGIHLNE	PHKTKRWGHSL	HFM
	e60 SSLPQDHIRG	ΣK			

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Figure 9:Patient B HBsAG sequence

MENITSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGTTVCLG QNSQSPTSNHSPTSCPPTCPGYRWMYLRRFIIFLFILLLCLIFLLVLLDY QGMLPVCPLIPGSSTTSTGPCRTCTTPAQGNSMYPSCCCTKPSDGNCTCI PIPSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWY WGPSLYRILSPFLPLLPIFFCLWVYI

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Figure 10: Patient C HBV NT sequence

10		30	40	50
CAGCAGCGCCTCCT		TCCAATCGGC	AGTCAGGAAGA	ACAGCCT
60	70	80	90	100
ACTCCCATCTCTCC	ACCTCTAAG	AGACAGTCATO	CCTCAGGCCA	TGCAGTG
110	120	130	140	150
GAACTCCAGCACAT	TCCACCAAG	CTCTGCTAGAT	CCCAGAGTG	AGGGGCC
160		180	190	200
TATATTTTCCTGCT		AGTTCCGGAAC	CAGTAAACCCI	GTTCCG
210		230	240	250
ACTACTGCCTCTCC		AATCTTCTCGA	.GGACTGGGGA	CCCTGC
260	270	280	290	300
ACCGAACATGGAGA	GCACCACATO	CAGGATTCCTA	.GGACCCCTGC	TCGCGT
310 TACAGGCGGGGTTT		330 ACAAGAATCCT		350 CAGAGT
360	370	380	390	400
CTAGACTCGTGGTG	GACTTCTCTC	CAATTTTCTAG	GGGGAACACC	CAAGTG
410	420	430	440	450
TCCTGGCCAAAATT	FGCAGTCCCC	CAACCTCCAAT	CACTCACCAA	CCTCTT
460 GTCCTCCAATTTGTC	470 CCTGGTTATC			500 TTTATC
510 ATCTTCCTCTTCATO		530 TGCCTCATCT		550 TCTTCT
560	570	580	590	600
GGACTACCAAGGTAT	GTTGCCCGT	TTGTCCTCTA	CTTCCAGGAA	CATCAA
610	620	000	640	650
CTACCAGCACGGGAC	CATGCAAGA		FCCTGCTCAA	GGAACC
660	670	680	690	
TCTATGTTTCCCTCT	TGTTGCTGT	ACAAAACCTTO	CGGACGGAAA	

710	720	730	740	750
TTGTATTCCC	ATCCCATCATC'	TTGGGCTTTC	GCAAGATTC	CTATGGGAGT
760		780	790	800
GGGCCTCAGT	CCGTTTCTCCT(GGCTCAGTTT	ACTAGTGCC	ATTTGTTCAG
810		830	840	850
TGGTTCGTAG	GGCTTTCCCCC2	ACTGTTTGGC	TTTTAGTTA	TATGGATGAT
860			890	900
GTGGTATTGG	GGGCCAAGTCT	GTACAACAYC	TTGAATCCCT	TTTTTACCGC
910	920	930	940	950
TGTTACCAAT	TTTCTTTTGTCT	TTGGGTATA	CATTTAAACO	CTACTAAAA
960		980	990	1000
CCAAACGTTG	GGGCTACTCCCT	TAACTTCAT	GGGATATGT	ATTGGAAGT
1010		1030	1040	
TGGGGTACCT"	TACCACAAGAAC	CATATTGTAC	ACAAAATCAG	GACAA

Figure 10 continued

Figure 11: Patient C Polymerase sequence

10	20	30	40	50
EDWGPCTEHGE	HHIRIPRTPARVI	rggvflvdkni	PHNTTESRLVV	DFSQFS
BCMTOVSWPKE	70 AVPNLQSLTNLLS	80	90	100
WOM I ON I WE	YA EMPÖDÜL MITIC	OTICT MCTUC.	ASAAT IUUPU	PAAMPH
110	120	130	140	150
TTAGSSGTLKX	VARLSSTSRNINY	(QHGTMQDLHI	DSCSRNLYVSL	LLLYKT
160	170	180	190	200
LGKKIHILISHE	IILGFRKIPMGVG	PLOPELLIAGE	"SAICSVVRRA	FPHCLA
210	220	230	240	250
FSIMDDVVLGA	KSVQHLESLFTAV	TNETTSTGIE	ILNPTKTKRWG	YSLNFM
260 GYVIGSWGTLP	270 QEHIVHKIRQ	-		

Figure 11

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Figure 12 Patient C HbsAg sequence

MESTTSGFLGPLLALQAGFFLLTRILTIPQSLDSWWTSLNFLGGTPKCPG QNLQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLWGLLDY QGMLPVCPLLPGTSTTSTGPCKTCTTPAQGTSMFPSCCCTKPSDGNCTCI PIPSSWAFARFLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLLVIWMMWY WGPSLYNXLNPFLPLLPIFFCLWVYI

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Figure 13; Patient D NT sequence

10	20	30	40	50
CTCCTGCATCTA	CCAATCGGCAGT	CAGGAAGAC	AGCCTACTCC	CATCTCT
60	70	80	90	100
CCACCTCTAAGA	GACAGTCATCCT		CAGTGGAACTC	ממסמר
			001001101	CHCHAC
110	120	130	140	150
	TCTGCTAGATCC		CCCCCTCTVTT エュロ	
	TOTOOTHORICO	DAD I DADOO	GGGCCICIAII	TICCIG
160	170	180	190	
CTGGTGGCTCCA		TOO	T 3.0	200
Olddiddcidda	GI I CCGGGACAG	TAAACCCTG	TTCCGACTACT	GCCTCT
210	220	220	0.40	0.50
		230	240	250
CCCATATCGTCA	ATCTTCTCGAGG	ACTGGGGAC	CCTGCACTGA	CATGGA
260	070	000		
260	270		290	300
GAGCACAACATC	AGGATTCCTAGG	ACCCCTGCT	CGTGTTACAGO	CGGTGT
212				
310			340	350
TTTTCTTGTTGA	CAAGAATCCTCA	CAATACCAC	AGAGTCTAGAC	TCGTGG
360			390	400
TGGACTTCTCTC	AATTTTCTAGGG	GAAGCACCC	GCGTGTCCTGG	CCAAAA
410	420	430	440	450
TTCGCAGTCCCC				СААТТТ
460	470	480	490	500
GTCCTGGCTATC				
		- 00000011		CICIIC
510	520	530	540	550
ATCCTGCTGCTA			℧℄℧ℼℼℼ	2277
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		1101100110	JIICIGGAIIA	CCAAGG
560	570	580	E 0.0	600
TATGTTGCCCGT	┻ ₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	JOU TCCDCCDDC	590	
INIGIT GCCCGI	IIGICCICIACI.	CCAGGAACC	STCAACTACCA	GCACGG
610	C20	620	640	
	620	630	640	650
GACCATGCAAGA	CUTGUAUGATTU	CTGCTCAAGG	SAACCTCTATG	TTTCCC
660	68.0			
660	670	680	690	700
TCATGTTGCTGT	ACAAAACCTTCG(JACGGAAACI	GCACTTGTAT	TCCCAT
			•	
	720-	- 730 -		-750
CCCATCATCCTG	GGCTTTCGCAAG	ATTCCTATGO	GAGTGGGCCT	CAGTCC

Figure 13

· 7	60	770	780	790	800
GTTTCTCT	TGACTCAGT	TTACTAGTGC	CATTTGTTCA	AGTGGTTCGT	\GGG
	10 CACTGTTT(820 GCTTTCAGTT		840 ATGTGGTATTO	850 GGG
_	60 TGTACAAC <i>A</i>	870 ATCTTGAGTCC	880 CTTTATACCG	890 CTATTACCA	900 ATTT
-	10 CTTTGGGT <i>I</i>	920 ATACATTTAAA	930 .СССТААТААА	940 ACCAAGCGAT	950 'GGG
_	60 CTTAACTTC	970 ATGGGATATG	980 TCATTGGAAG		.000 TTA
10: CCACAGGA	- · -	.020 'GCTC			

Figure 13 continued

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Figure 14: patient D HBV POL sequence

EDWGPCTEHGEHNIRIPRTPARVTGGVFLVDKNPHNTTESRLVVDFSQFS RGSTRVSWPKFAVPNLQSLTNLLSSNLSWLSLDVSAAFYHLPLHPAAMPH ${\tt LLVGSSGLPRYVARLSSTSRNVNYQHGTMQDLHDSCSRNLYVSLMLLYKT}$ ${\tt FGRKLHLYSHPIILGFRKIPMGVGLSPFLLTQFTSAICSVVRRAFPHCLA}$ FSYMDDVVLGAKSVQHLESLYTAITNFLLSLGIHLNPNKTKRWGYSLNFM GYVIGSWGTLPQEHIVL

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Figure 15 Patient D HBsAg sequence

MESTTSGFLGPLLVLQAVFFLLTRILTIPQSLDSWWTSLNFLGEAPACPG QNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDY QGMLPVCPLLPGTSTTSTGPCKTCTIPAQGTSMFPSCCCTKPSDGNCTCI PIPSSWAFARFLWEWASVRFS*LSLLVPFVQWFVGLSPTVWLSVIWMMWY WGPSLYNILSPFIPLLPIFFCLWVYI

Figure	16:	Patient	E	HBV	nt	sequence
--------	-----	---------	---	-----	----	----------

rigure	10.	racten	LE	пьч	nt	seq	ience			
	10		20			30		40		50
AGTCATO	CCTCA	AGGCCAT	GCAG	STGGA	ACT	'CCA	CACA	TCCA	CCAAG	CTCT
	60		70			80		90		100
GCTAGAT	CCCA	LGAGTGA	.GGGG	CCTA	TAC	TTT(CCTGCT	GGTG	GCTCC	AGTT
	110				1	30		140		150
CAGGAAC	CAGTA	AACCCT	GTTC	CGAC	TAC	TGC	CTCTCC	CATA	TCGTC	AATC
mm à ma car	160		170		1			190		200
TTCTCG	AGGAC	TGGGGA	CCCI	GCAC	CGA	ATA:	GGAGA	AGCAC	CACATO	CAGG
3 MM C C M 3	210		220		2	30		240		250
ATTCCTA	IGGAC	CCCTGC	TCGT	'GTTA	CAG	GCGG	GGTTI	TTCT	TGTTG	ACAA
СДДПССТ	260	እ ሞአ <i>ርር</i> አ	270	CMCM	2	80 60	macma	290	mamama	300
GAATCCT	CACA	AIACCA	CAGA	GTCT.	AGA	CTCG	TGGTG	GAC'I"	TCTCTC	TAAT
TTTCTAG	310 :cccc		320 CCCC	THCTHC	3	30	חות הה	340	amaaaa	350
11101110							MAATI	IGCA	GTCCCC	AAC
ርጥሮር እ አጥ	360			mmem				390		400
CTCCAAT	CACI	CACTAA						CCTG	GTTATC	GCT
CORMONO	410		420		4	30		440		450
GGATGTG	TCTG	CGGCGT	ГТТА	TCAT	CTT	CCTC	TTCAT	CCTG	CTGCTA	TGC
	460					80		490		500
CTCATCT	TCTT	GTTGGT'	FCTT	CTGG	ACT	ACCA	AGGTA	TGTT	GCCCGI	TTG
	510							540		550
TCCTCTA	CTTC	CAGGAA	JATC.	AACTA	ACC	AGCA	CGGGA	CCAT	GCAAGA	CCT
		CCIIICAA		aamar			aaama	590		600
GCACGAC	TCCT	GCTCAA	3GAA			3'I'I'I	CCCTC	TTGTT	rgttgt	ACA
	610		520			30		640		650
AAACCTT	CGGA	UGGAAA'.	rtgc	ACTTO	STAT	rtcc	CATCC	CATC	ATCTTG	GGC
	660	(570		68	30				700
TTTCGCA	AGAT:	rcctat(GGA	GTGGG	GCC1	rcag	TCCGT'	TTCTC	CATGGC	TCA

Figure 16

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710 720 730 740 750 ${\tt GTTTACTAGTGCCATTTGTTCAGTGGTTCGTAGGGCTTTCCCCCACTGTT}$ 770 780 TGGTTTTCAGTTATGTGGATGATGTGGTATTGGGGGCCAAGTCTGCACAA 820 830 CATCTTGAATCCCTTTTTACCGCTATTACCAATTTTCTTTTGTCTTTGGG 870 880 TATACATTTAAACCMTAATAAAACCAAACGTTGGGGCTATTCCCTTAACT 910 920 930 TTATGGGATATGGAATTGGAAGTTGGGGTCCTGCCCAGGGAAGATGGCAG GGG

Figure 16 continued

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Figure 17 Patient E: HBV polymerase

20 30 ${\tt SSSGHAVELQHIPPSSARSQSEGPILSCWWLQFRNSKPCSDYCLSHIVNL}$ 80 . 90 ${\tt LEDWGPCTEYGEHHIRIPRTPARVTGGVFLVDKNPHNTTESRLVVDFSQF}$ 130 140 ${\tt SRGSTRVSWPKFAVPNLQSLTNLLSSNLSWLSLDVSAAFYHLPLHPAAMP}$ 170 180 190 ${\tt HLLVGSSGLPRYVARLSSTSRNINYQHGTMQDLHDSCSRNLYVSLLLLYK}$ 220 230 240 TFGRKLHLYSHPIILGFRKIPMGVGLSPFLMAQFTSAICSVVRRAFPHCL 260 270 280 290 VFSYVDDVVLGAKSAQHLESLFTAITNFLLSLGIHLNXNKTKRWGYSLNF MGYGIGSWG

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Figure 18: Patient E HBsAg

WO 2005/042733

20 30 40 QPTPISPPLRDSHPQAMQWNSSTFHQALLDPRVRGLYFPAGGSSSGTVNP 70 80 VPTTASPISSIFSRTGDPAPNMESTTSGFLGPLLVLQAGFFLLTRILTIP 120 130 140 QSLDSWWTSLNFLGGAPACPGQNLQSPTSNHSLTSCPPICPGYRWMCLRR 180 190 FIIFLFILLLCLIFLLVLLDYQGMLPVCPLLPGTSTTSTGPCKTCTTPAQ 220 230 240 GTSMFPSCCCTKPSDGNCTCIPIPSSWAFARFLWEWASVRFSWLSLLVPF 280 290 VQWFVGLSPTVWFSVMWMMWYWGPSLHNILNPFLPLLPIFFCLWVYI*TX IKPNVGA

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Figure 19: Patient F: nt sequence

rigure	19:	Patient	t F:	nt	sequence		
	10)	20		30	40	50
CCAATO	CGGC	AGTCAGG	AAGA	CAG	CCTACTCCCA	ATCTCTCCAC	CTCTAAGA
	60	1	70		0.0	0.0	
GACAGI			CAT	GCA	8U TGGAACTCO	90 CAGCACATTC	100 Caccaacc
							CACCAAGC
mamaa	110		120		130	140	150
TCTGCT	'AGA'I	CCCAGAC	STGA	GGG	SCCTATACTI	TCCTGCTGG	TGGCTCCA
	160)	170		180	190	200
GTTCCG	GAAC	CAGTAAAC	CCT	GTTC	CCGACTACTO	CCTCTCCCA	TATCGTCA
	210	,	220		000	0.40	
АТСТТС					230	240 ATGGAGAGC	
		100110100	OOA		GCACCGAAI	AIGGAGAGC	ACCACATO
)	270		280	290	300
AGGATT	CCTA	GGACCCC	TGC	rcg1	GTTACAGGC	GGGGTTTTT	CTTGTTGA
	310)	320		330	340	350
CAAGAA			CCA	CAGA	GTCTAGACT	CGTGGTGGA	CTTCTCTC
* * * * * * * * * * * * * * * * * * * *	360		370		380	390	400
AATTTT	CTAG	IGGGGAGC	ACC	CACG	STGTCCTGGC	CAAAATTTG	CAGTCCCC
	410		420		430	440	450
AACCTC	CAAT	CACTCAC	CAAC	CCTC	TTGTCCTCC	AATTTGTCC	TGGTTATC
	460		470		400	400	500
GCTGGA		TCTGCGG	ፋ 7 U ICGTT	ነጥጥ ልጥጥ፣	480 TCATCTTCC	490 TCTTCATCC	500 TGCTGCTA
							TOOLGGIA
	510		520		530	540	
TGCCTC	ATCT	TCTTGTT	GGTI	CTT	CTGGACTAC	CAAGGTATG'	PTGCCCGT
	560		570		580	590	600
TTGTCC			GAAC	ATC	AACTACCAG	CACGGGACC	ATGCAAGA
00000	610	maa====	620		630	640	650
CCTGCA	CGAC	TCCTGCT	CAAG	GAA	CCTCTATGT	TTCCCTCTT	STTGCTGT

Figure 19

660	670	680	690	700
ACAAAACCTTCGGAC	GGAAATTGCA	CTTGTATTCC	CATCCCATCA	TCTTG
710	720	730	740	750
GGCTTTCGCAAGATT	CCTATGGGAG'	rgggcctcag	TCCGTTTCTC	CTGGC
760		780	790	800
TCAGTTTACTAGTGC	CATTTGTTCA	GTGGTTCGTA	GGGCTTTCCC	CCACT
810		830	840	850
GTTTGGCTTTCAGTT	ATATGGATGA	GTGGTATTG	GGGGCCAAGT	CTGTA
860	870	880	890	900
CAACATCTTGAATCC	CTTTTTACCG	CTGTTACCAA	PTTTCTTTTG	TCTTT
910	920	930	940	950
GGGTATACATTTAAA	CCTACTAAAA	ACTAAACGTT(GGGCTACTC	CCTTA
960	970	980		
ACTTCATGGGATATG	TAATTGGAAG1	TGGGGTACC	ГТG	

Figure 19 continued

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Figure 20 Patient F Pol Amino acid sequence

10 20 30 40 EDWGPCTEYGEHHIRIPRTPARVTGGVFLVDKNPHNTTESRLVVDFSQFS 70 80 90 100 RGSTHVSWPKFAVPNLQSLTNLLSSNLSWLSLDVSAAFYHLPLHPAAMPH 120 130 140 LLVGSSGLPRYVARLSSTSRNINYQHGTMQDLHDSCSRNLYVSLLLLYKT 180 190 FGRKLHLYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVRRAFPHCLA 210 220 230 240 . 250 FSYMDDVVLGAKSVQHLESLFTAVTNFLLSLGIHLNPTKTKRWGYSLNFM GYVIGSWG

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Figure 21 Patient F HBsAg seq

MESTTSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGAPTCPG QNLQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDY QGMLPVCPLLPGTSTTSTGPCKTCTTPAQGTSMFPSCCCTKPSDGNCTCI PIPSSWAFARFLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWY WGPSLYNILNPFLPLLPIFFCLWVYI

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Figure 22: Patient G ; HBV nt

rigure	22:	Patien	t G	; HBV n	it				
ጥርርርር	10		20) AMCCCC	30		40		50
100000	. I CC 1	GCCTCC	ACCA	MICGCC	AGTC	AGGAAG	GCAAC	CTACC	CGC
ጥ ርጥርጥ <i>ር</i>	60		70) ''''	80		90		100
101010	CACC	TTTGAG	AUAC	ACTCAT	CCTC	AGGCCG:	rgcag	TGGAAC	TCC
	110		120)	130		140		150
ACAACO	CTTCC	CACCAAA	CTCI	'GCAAGA	TCCC	AGAGTG	AGGGG	CCTGTA	TCT
	160		170)	180		190		200
CCCTGC	TGGI	GGCTCC	AGTI	'CAGGAA	CAGC	AAACCC:	rgttc	CGACTA	CTG
	210		220	ŀ	230		240		250
CCTCTC	CCTI	ATCGTC	AATC	TTCTCG	AGGA'	rtgggg <i>i</i>	ACCCT	GCGCTG	AAC
	260	1	270	ı	280		290		300
ATGGAG	SAACA	TCACATO	CAGG	ACTCCT	AGGA	CCCTT	CTCGT	GTTACA	GGC
	310		320	ı	330		340		350
GGGGTT		TTGTTG	ACAA	GAATCC	TCAC	ATACCO	GCAGA	GTCTAG	ACT
CGTGGT		TTCTCTC		ጥጥጥርጥል					400
								101011	GGC
~	410		420						450
CAAAAT	TCGC	GGTCCCC	CAAC	CTCCAA	TCACT	CACCA	ACCTC	CTGTCC	TCC
	460		470		480		490		500
GACTTG	TCCT	GGTTATC	CGCT	GGATGT.	ATCT	CGGCGI	TTTA	ICATAT	TCC
	510		520		530		540		550
TCTTCA	TCCT	GCTGCTA	TGC	CTCATC	TTCTT	GTTGGT	TCTT	CTGGAC	TAT
	560		570		580		590		600
CAAGGT	ATGT	TGCCCGI	TTG	TCCTCT	AATTC	CAGGAT		AACCAC	CAG
	610		620		630		640		650
CACGGG		TGCCGAA					GGAA	CCTCTA	
ATCCCT	660 CCTG	TTGCTGT	670 ACC	AAACCT	680 PCGGA	CGGAAA	690 TTGC	ACCͲϾͲ	700 ልጥጥ

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710			740	750
CCCATCCCATC	ATCTTGGGCTTT	CGGAAAATTC	CTATGGGAGT	GGCCTC
760		780	790	800
AGCCCGTTTCT	CCTGGCTCAGTT	TACTAGTGCC	ATTTGTTCAG:	rggttcg
810			840	850
TAGGGCTTTCC	CCCACTGTTTGG	CTTTCAGTTA:	PATGGATGAT(STGGTAT
860		880	890	900
TGGGGGCCAAG	TCTGTACAGCAT	CTTGAGTCCC:	TTTTACCGC	TGTTACC
910		930	940	950
AATTTTCTTTT	GTCTTTGGGTAT	ACATTTAACC	CCTAACAAAA	CAAAGAG
960		980	990	1000
ATGGGGTTACT	CTCTAAATTTTA:	rgggctatgt(CATTGGAAGTT	TATGGGT
1010	1020	1030	1040	
CCTTGCCACAA	GAACACATTATA	CTAAAAATCA	AGATTGTTT	

Figure 22 continued

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Figure 23 Patient G HBV POL

20 30 EDWGPCAEHGEHHIRTPRTPSRVTGGVFLVDKNPHNTAESRLVVDFSQFS 70 80 RGNYRVSWPKFAVPNLQSLTNLLSSDLSWLSLDVSAAFYHIPLHPAAMPH 120 130 LLVGSSGLSRYVARLSSNSRILNHQHGNMPNLHDSCSRNLYVSLLLLYQT 170 180 ${\tt FGRKLHLYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVRRAFPHCLA}$ 220 230 240 FSYMDDVVLGAKSVQHLEŞLFTAVTNFLLSLGIHLTPNKTKRWGYSLNFM GYVIGSYG

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Figure 24: Patient G HbsAg

WGPSLYSILSPFLPLLPIFFCLWVYI

10 20 30 40 50

MENITSGLLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLSFLGGTTVCLG

60 70 80 90 100

QNSRSPTSNHSPTSCPPTCPGYRWMYLRRFIIFLFILLLCLIFLLVLLDY

110 120 130 140 150

QGMLPVCPLIPGSSTTSTGTCRTCTTPAQGTSMYPSCCCTKPSDGNCTCI

160 170 180 190 200

PIPSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWY

210 220

Figure 24

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Figure 25 Patient H nt seq

10	20	30	40	50
CGCCTCCTGCC	TCCACCAATCGCC	AGTCAGGAA	GGCAGCCGAC	CCCACTG
60	70	80	90	100
TCTCCACCTTT	'GAGAGACACTCAT	CCTCAGGCC	GTGCAGTGGA <i>I</i>	ACTCCAC
110	120	130	140	150
AACCTTCCACC	AAACTCTGCAAGA	TCCCAGAGTO	GAGAGGCCTGT	TATTTCC
160	170		190	200
CTGCTGGTGGC	TCCAGTTCAGGAA		CTGTTCCGACO	CACTGCC
210	220		240	250
TCTCCCTTATC	GTCAATCTTCTCG		SACCCTGCGCT	GAACAT
260	270	280		300
GGAGAACATCA	CATCAGGATTCCT	AGGACCCCTI		AGGCGG
310	320	330		350
GGTTTTTCTTG	TTGACAAGAATCC	TCACAATACO		GACTCG
360 TGGTGGACTTC	370 TCTCAGTTTTCTA			400 TGGCCA
410	. 420	430	440	450
AAATTCGCAGT	CCCCAACCTCCAA	TCACTCACC	ACCTCCTGTC	CTCCAA
460 CTTGTCCTGGT	470 FATCGCTGGATGT	480 GTCTGCGGCG		
510	520	530		550
TTCATCCTGCT	GCTATGCCTCATC	TTCTTGTTGG		CTATCA
560	570		590	600
AGGTATGTTGC	CCGTTTGTCCTCT		TCCTCAACCA	CCAGCA
610 CGGGACCATGC	620 CGAACCTGCACGA			
660 CCCTCCTGTTG	670 CTGTACCAAACCT			700 TATTCC

Figure 25

710		730	740	750
CATCCCATCATCTT	GGGCTTTCG	CAAAATTCCTA	ATGGGAGTGG	GGCTCAG
760	770	. 700	500	
·			790	800
CCCGTTTCTCATGG	CTCAGTTTA	CTAGTGCCATI	TGTTCAGTG	STTCGTA
810	820	830	0.40	0.5.0
- -			840	850
GGGCTTTCCCCCAC	TGTTTGGCT	I'I'CAGTTATGI	GGATGATGT(GTAŢTG
9.60	070	000		
			890	900
GGGGCCAAGTCTGT	ATCGCATCT'	IGAGTCCCTTT	TTACCGCTGT	TACCAA
910			940	950
TTTTCTTTTGTCTT	TGGGTATAC	ATTTAAACCCT	'AACAAAACGA	AAAAGAT
960	970	980	990	1000
GGGGTTACTCTTTA	AATTTTATGO	GGTATGTTAT	TGGATGTTAT	GGGTCC
1010	1020			
TTGCCACAAGAACA	CATCGTACA	AAA		

Figure 25 continued

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Figure 26: Patient H HBV pol

20 30 40 EDWGPCAEHGEHHIRIPRTPSRVTGGVFLVDKNPHNTAESRLVVDFSQFS 80 90 ${\tt RGNHRVSWPKFAVPNLQSLTNLLSSNLSWLSLDVSAAFYHIPLHPAAMPH}$ 120 130 140 LLVGSSGLSRYVARLSSNSRILNHQHGTMPNLHDSCSRNLYVSLLLLYQT 170 180 190 ${\tt FGRKLHLYSHPIILGFRKIPMGVGLSPFLMAQFTSAICSVVRRAFPHCLA}$ 220 230 240 FSYVDDVVLGAKSVSHLESLFTAVTNFLLSLGIHLNPNKTKRWGYSLNFM GYVIGCYGSLPQEH

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Figure 27: Patient H HBsAg

20 30 40 MENITSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLSFLGETTVCLG 70 80 QNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLIFLLVLLDY 120 130 QGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCI 170 180 190 200 PIPSSWAFAKFLWEWGSARFSWLSLLVPFVQWFVGLSPTVWLSVMWMMWY 210 220 WGPSLYRILSPFLPLLPIFFCLWVYI

Figure 28 Patient I HBV nt seg

Figure 28 Patien	t I HBV nt	seq		
10 CAACTTGTCCTGGTTA	20 TCGCTGGATG		40 CGTTTTATCA	50 TATTC
60 CTCTTCATCCTGCTGC	70 TATGCCTCAT	80 CTTCTTGTT	90 GGTTCTTCTG	100 GACTA
110 TCGAGGTATGTTGCCC	120 GTTTGTCCTC	130 TACTTCCAGO		
160 GCACGGGTCCATGCAG	170 AACCTGCACG	180 ACTCCTGCT		
210 TATCCCTCATGTTGCT		230 TTCGGACGG		
260 TCCCATCCCATCATCC	270 TGGGCTTTCG	280 Gaaaattcci		
310 CAGCCCGTTTCTCATG	320 GCTCAGTTTA			
360 GTAGGGCTTTCCCCCA	370 TTGTTTGGCT			
410 TTGGGGGCCAAGTCTG		430 TGAGTCCCTI		
460 CAATTTTCTTTTGTCT	470 CTGGGTATAC		490 CTCACAAAAC	
510 GATGGGGTTACTCTTT		530 GGCTATGTC <i>F</i>		
560 TCTTTGCCAC				

Figure 28

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Figure 29 Patient I HBV pol

NLSWLSLDVSAAFYHIPLHPAAMPHLLVGSSGLSRYVARLSSTSRIFNHQ ${\tt HGSMQNLHDSCSRNLYVSLMLLYQTFGRKLHLYSHPIILGFRKIPMGVGL}$ ${\tt SPFLMAQFTSAICSVVRRAFPHCLAFSYVDDVVLGAKSVSHLESLFTAVT}$ NFLLSLGIHLNPHKTKRWGYSLHFMGYVIGCYGSLP

Figure 29

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Figure 30 Patient I: HBsAg

10 20 30 40 50
TCPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYRGMLPVCPLLPGSSTTS

60 70 80 90 100
TGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPIPSSWAFGKFLWEWAS

110 120 130 140 150
ARFSWLSLLVPFVQWFVGLSPIVWLSVMWMMWYWGPSLYRILSPFLPLLP

160 170 180
IFFCLWVYI*

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Figure 31

71	-	720	730	740	750
CCCATCCCA	TCATCTTO	GGCTTTCGC	AGATTCCTAT	rgggagtgg	GCCTC
76		770	780	790	800
AGTCCGTTT	CTCCTGGC	TCAGTTTACI	PAGTGCCATT	GTTCAGTG	STTCG
81	-		830		850
TAGGGCTTT	CCCCACT	'GTTTGGCTT1	CAGTTATATO	GATGATGT	GTAT
86	0	870	880	890	900
TGGGGGCCA	AGTCTGTA	CAACATCTTC	SAATCCCTTTI	TACCGCTGT	TACC
91	0	920	930	940	950
AATTTTCTT	TTGTCTTT	GGGTATACAT	TTAAACCCTA	CTAAAACTA	AACG
96	0	970	980	990	1000
TTGGGGCTA	CTCCCTTA	ACTTCATGGG	ATATGTAATI	GGAAGTTG	GGTA
101	0 1	020			
CCTTACCAC	AGGAACAT	ATTGTACACA	AA		

Figure 31 continued

Figure 32 Patient J HBV pol

20 30 EDWGPCTEYGEHNIRIPRTPARVTGGVFLVDKNPHNTTESRLVVDFSQFS 70 80 RGSTHVSWPKFAVPNLQSLTNLLSSNLSWLSLDVSAAFYHLPLHPAAMPH 120 130 $\verb|LLVGSSGLPRYVARLSSTSRNINYQHGTMQDLHDSCSRNLYVSLLLLYKT|$ 170 180 190 ${\tt FGRKLHLYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVRRAFPHCLA}$ 230 240 ${\tt FSYMDDVVLGAKSVQHLESLFTAVTNFLLSLGIHLNPTKTKRWGYSLNFM}$

260 GYVIGSWGTLPQEHIVHK

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Figure 33. Patient J HBsAg

10 20 30 40 50 MESTTSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGAPTCPG

60 70 80 90 100 QNLQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLXVLLDY

110 120 130 140 150 QGMLPVCPLLPGTSTTSTGPCKTCTIPAQGTSMFPSCCCTKPSDGNCTCI

160 170 180 190 200 PIPSSWAFARFLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWY

210 220 WGPSLYNILNPFLPLLPIFFCLWVYI

Figure 33

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Figure 34 Patient K HBV nt

ragure	od racienc	. K ABV IIC			
СТССТС	10 CTGCCTCCAC	20 CAATCGGCAG	30	40	50
-10010	01 000 1 00.10	0.11.11.0000110) ADAMDDAO 1	AGCCIACACC	CAIC
momoca.	60	70	80	90	100
ICICCA	CCTCTAAGAG	ACAGTCATCC	TCAGGCCATG	CAGTGGAACT	'CCAG
	110	100	100		
C n C n mm	110	120	130	140	150
CACATT	CCACCAAGCT	CTGCTAGATO	CCAGAGTGAG	GGGCCTATAC	TTTC
	160	170	7.00		
CBCCBC		1/0	180	190	200
CTGCTGC	GTGGCTCCAG	TTCAGGAACA	GTAAACCCTG	TTCCGACTAC	TGCC
	210	220	230	240	0.50
тстссс		CCU CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	23U	240	250
1010002	HIAICGTCAA	TCTTCTCGAG	GACTGGGGAC	CCTGCACCGA	ATAT
	260	270	200	290	
CCRCRC		2/0	280	290	300
GGAGAGG	CACCACATCA	GGATTCCTAG	GACCCCTGCT	CGTGTTACAG	GCGG
	310	330	330	240	250
CCmmmm		320 77677866	330	340	350
GGIIII	ICTIGITGAC.	AAGAATCCTC	ACAATACCAC	AGAGTCTAGA	CTCG
	360	370	300	300	400
тестест	♪₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	ATTTTCTAGG		390	400
1001002	CITCICICA	MITITOTAGG	GGGAGCACCC	ACGTGTCCTG	GCCA
	410	420	430	440	450
AAATTTC		ACCTCCAATC	TOU TOUCHOUND	CUCUUCUCCU	420
	301101000011	ilooi cchric.	NO I CACCAAC	CICIIGICCI	CCAA
	460	470	480	490	500
TTTGTCC		CTGGATGTGT	CTGCGGCGTT	™™₯₼₼₼₼₼ ₼₼₯₼₼	
		01001110101	0100000011	ITAICAICII	CCIC
	510	520	530	540	550
TTCATCO	TGCTGCTAT	GCCTCATCTT(ĊŢŢĠŢŢŢĠŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢ	C™™C™CCXC™	7007
			0110110011	OIICIGGACI.	ACCA
	560	570	580	590	600
AGGTATO	TTGCCCGTT	TGTCCTCTAC:	TTCCAGGNAC	ろうひ カጥሮカ カで切み <i>でで</i>	7007
		10100101110	I I CONGGAAC.	AI CAACIACO	AGCA
	610	620	630	640	650
CGGGACC		CTGCACGATT	ってむらしかしなる。	ころろととかとのみの	
			CICCICAAG	OFFICCI CIMI	3111
	660	670	680	690	700
CCCTCTT	ġŢŢĠĊŢĠŢ <u>Ŏ</u>	CAAAACCTTC	こここ	・ でころんしかからのかり	יטטי דייירכי
			CUCCOUNT	CONCILCIA	1100

Figure 34

	710	720	730	740	750
CATCCCA	TCATCTTGG	GCTTTCGCAA	GATTCCTATG	GGAGTGGGCC	TCAG
	760	770	780	790	800
TCCGTTT	CTCCTGGCT	CAGTTTACTA	GTGCCATTTG'	TTCAGTGGT	CGTA
	810	820	830	840	850
GGGCTTT	CCCCCACTG	TTTGGCTTTC	AGTTATATGG	ATGATGTGGT	ATTG
	860	870	880	890	900
GGGGCCA	AGTCTGTAC	AACATCTTGA	ATCCCTTTTT	ACCGCTGTT	ACCAA
	910	920	930	940	950
TTTTCTT	TTGTCTTTG		TAAACCCTRC	TAAAACCAA	ACGTT
	960	970	980	990	1000
GGGGTTA	CTCCCTTAA		TATGTAATTG	GAAGTTGGG	STACC
•					
·1	.010	1020	1030		
TTACCAC	CAGGAACATA	TTGTACACA	AATCAAACA		

Figure 34 continued

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Figure 35 Patient K HBV pol

20 30 SSCLHQSAVRKTAYTHLSTSKRQSSSGHAVELQHIPPSSARSQSEGPILS CWWLQFRNSKPCSDYCLSHIVNLLEDWGPCTEYGEHHIRIPRTPARVTGG 130 VFLVDKNPHNTTESRLVVDFSQFSRGSTHVSWPKFAVPNLQSLTNLLSSN 170 180 LSWLSLDVSAAFYHLPLHPAAMPHLLVGSSGLPRYVARLSSTSRNINYQH 220 230 GTMQDLHDSCSRNLYVSLLLLYKTFGRKLHLYSHPIILGFRKIPMGVGLS 270 280 290 PFLLAQFTSAICSVVRRAFPHCLAFSYMDDVVLGAKSVQHLESLFTAVTN 320 330 FLLSLGIHLNPXKTKRWGYSLNFMGYVIGSWGTLPQEHIVHKIK

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Figure 36 Patient K HbsAg

PPASTNRQ	10 SGRQPTPIS	20 PPLRDSHPQA		40 ALLDPRVRGL	50 YFP
AGGSSSGA		70 PISSIFSRTG		90 SGFLGPLLVL	100 QAG
		120 WTSLNFLGGA		140 SPTSNHSPTSC	150 PPI
		170 'ILLLCLIFLI		190 PVCPLLPGTST	200 TST
	210 IPAQGTSMFF	220 SCCCTKPSDG	230 ENCTCIPIPS	240 SWAFARFLWEW	250 IASV
RFSWLSLI	260 LVPFVQWFVG	270 LSPTVWLSVI	280 WMMWYWGPSI	290 LYNILNPFLPI	7751 300
	310 I*TLLKPNVO	320 SVTPLTSWDM ³	330 LEVGVPYHRI		

Figure 36

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Figure 37 Patient L HBV nt

10	20	30	40	50
CAGTCCGGAAGGCAGCC	CTACTCCCTT	ATCTCCACCT	CTAAGGGACA	CTCA
60	70	80	90	100
TCCTCAGGCCATGCAGT	GGAACTCCA	CCACTTTCCA:	PCAAACTCTT	ÇAAG
110	120	130	140	150
ATCCCAGAGTCAGGGCT	CTGTACTTT	CCTGCTGGTG	SCTCCAGTTC	AGGA
160			190	200
ACAGTGAGCCCTGCTCA	AGAATACTGC	CTCTGCCATA!	PCGTCAACCT'	rcrc
210	220	220	240	250
GAAGACTGGGGACCCTG				
GAAGAC1GGGGACCC1G	TACCGAACA.	GGAGAACAT	JGCA I CAGGA	CICC
260	270	280	290	300
TAGGACCCCTGCTCGCC	TTACAGGCG	366 44444	CGTTGACAAA	AATC
310	320	330	340	350
CTCACAATACCACAGAG				
360	370	380	390	400
AGGGGGAACACCCGTGT	GTCTTGGCC	AAAATTCGCA	GTCCCAAATC'	rcca
	420			
GTCACTCACCAACTTGT	TTGTCCTCCA	ATTTGTCCTG	GTTATCGCTG(GATG
	470			500
TGTCTGCGGCGTTTTAT	CATCTTCCT	CTGCATCCTG	CTGCTATGCC	l'CAT
E10	520	E 2.0	T 40	E E A
CTTCTTGTTGGTTCTTC				
CITCITGITGGITCITC	JIGGACIAICA	ANGGINIGIII	3CCCG111G1	CIC
560	570	580	590	600
TAATTCCAGGATCATCA				
610	620	630	640	650
ACTCCTGCTCAAGGAAC				

Figure 37

660	670	680	690	700
TACGGACGGAA	ACTGCACCTGT	ATTCCCATCCC	ATCATCTTGG(GCTTTCG
710			740	750
CAAAATACCTA	rgggagtgggc	CTCAGTCCGTT	rctcttggct(CAGTTTA
760	770	780	790	800
CTAGTGCCGTT	rgttcagtggt:	rcgtagggctt:	rccccactg'	TCTGGCT
		000	0.40	050
810			840	850
TTCAGTTATAT	GGATGATGTGG'	PATTGGGGGCC	AAGTCTGTAC	AACATCT
860	870	880	890	900
TGAGTCCCTTT	Δ ΨGCCGCΨGΨΨ)	ACCAATTTTCT'	TTTGTCTTTG	GGTATAC
IGAGICCCIII				
910	920	930	940	950
ATTTAAACCCT	CACAAAACAAA	AAGATGGGGAT.	ATTCCCTTCA	ATTCATG
960	970	980		
GGATATGTAAT	TGGGGGTTGGG	GCTCCTTG		

Figure 37 continued

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Figure 38. Patient L Pol

30 EDWGPCTEHGEHRIRTPRTPARVTGGVFLVDKNPHNTTESRLVVDFSQFS 70 80 RGNTRVSWPKFAVPNLQSLTNLLSSNLSWLSLDVSAAFYHLPLHPAAMPH 130 140 $\verb|LLVGSSGLSRYVARLSSNSRIINHQHRTMQNLHDSCSRNLYVSLMLLYKT|$ 180 190 ${\tt YGRKLHLYSHPIILGFRKIPMGVGLSPFLLAQFTSAVCSVVRRAFPHCLA}$ 220 230 240 ${\tt FSYMDDVVLGAKSVQHLESLYAAVTNFLLSLGIHLNPHKTKRWGYSLQFM}$ GYVIGGWG

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Figure 39 Patient L HBsAg

10 20 30 40 50

MENIASGLIGPLIALQAGFFSLTKILTIPQSLDSWWTSLNFLGGTPVCLG

60 70 80 90 100

QNSQSQISSHSPTCCPPICPGYRWMCLRRFIIFLCILLLCLIFLLVLLDY

110 120 130 140 150

QGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMFPSCCCTKPTDGNCTCI

160 170 180 190 200

PIPSSWAFAKYLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWY

210 220

WGPSLYNILSPFMPLLPIFFCLWVYI

	10	20	30	40	50
CCTGCTG	GTGGCTCCAG	TTCAGGAAC	AGTAAACCCTC	STTCCGACTAC	TGC
	60	70	80	90	100
СТСТССС			GATTGGGGA		
	110	120	130		150
TGGAGAA	CATCACATCA	AGGATTCCTAC	GACCCCTTCT	CGTGTTACAC	GCG
	160	170	180	190	200
GGGTTTT			CACAATACCG		
CMCCMCC	210	220	230 EGGGAACTAC	240	250
GTGGTGG	ACTICICICA	ATTTTCGAG	3GGGAACTAC(CGIGIGICII	3000
	260	270	280	290	300
AAAATTC	GCAGTCCCCA	ACCTCCAAT	CACTCACCAA	CCTCCTGTCCI	CCA
	21.0	320	220	340	250
ACTTGTC	310 :CTGGTTATC6	SZU CTGGATGTG	330 CTGCGGCGT	─────────────────────────────────────	
	,01001111100		.01000001		
	360	370	380	390	400
CTTCATC	CTGCTGCTAI	GCCTCATCT	CTTGTTGGT	rcttctggac1	PATC
	410	420	430	440	450
RAGGTAI			ATTCCAGGAT		
1000010			480		
ACGGGAC	CATGCCGAAC	COTGCATGAC	PACTGCTCAA(GAACCTCTA!	IGTA
	510	520	530	540	550
TCCCTCC	TGTTGCTGT	ACCAAACCTA	CGGACGGAAA	TTGCACCTGT#	ATTC
	5.60	550	500	500	600
CCNTCCC	560 ************************************		580 AAATTCCTAT(590	
CCATCCC	AICAICCIG	GCTTTCGGA	AMAI I CCIMI	JOGAG I GOGC	JION
			630		
GCCCGTI	TCTCCTGGCT	CAGTTTACT	AGTGCCATTT	GTTCAGTGGT	rcgt
	660	670	680	690	700
AGGGCTI			CAGTTATATG		
	710	720	730	740	750
GGGGGCC	CAAGTCTGTA	MGCATCTTG	AGTCCCTTTT	PACCGCTGTT?	ACCA
	760	770	780	790	800
ATTTTCI			TTAAACCCTA		GAGA
mccccm	810	820 \#####\###	830 PTATGTCATT	840 	850 2010
1666611	ACTOTOTOAA	ALLITATOGO,	ITAIGICATT	GUNGI INIG	3616
		870		890	900
CTTGCCA	CAAGAACAC	ATCATACAAA	AAATCAAAGA	ATGTTTTAGA!	AAAC

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CWWLQFRNSKPCSDYCLSLIVNLLEDWGPCAEHGEHHIRIPRTPSRVTGG VFLVDKNPHNTAESRLVVDFSQFSRGNYRVSWPKFAVPNLQSLTNLLSSN LSWLSLDVSAAFYHXPLHPAAMPHLLVGSSGLSRYVARLSSNSRILXHQH GTMPNLHDYCSRNLYVSLLLLYQTYGRKLHLYSHPIILGFRKIPMGVGLS PFLLAQFTSAICSVVRRAFPHCLAFSYMDDVVLGAKSVXHLESLFTAVTN FLLSLGIHLNPNKTKRWGYSLNFMGYVIGSYGSLPQEHIIQKIKECFRK

Figure 41

PAGGSSSGTVNPVPTTASPLSSIFSRIGDPALNMENITSGFLGPLLVLQA GFFLLTRILTIPQSLDSWWTSLNFRGGTTVCLGQNSQSPTSNHSPTSCPP TCPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYXGMLPVCPLIPGSSXTS TGPCRTCMTTAQGT\$MYPSCCCTKPTDGNCTCIPIPSSWAFGKFLWEWAS ARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYXILSPFLPLLP IFFCLWVYI*

Figure 42

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a======	10		30		50
CTTTCAC	CCAAACTCTGC	CAAGATCCCC	CTGCTGGTGG	CTCCAGTTCA	GGAA
САСТАА	60 ACCCTGTTCC	70 3acmacmacc			100
011011111					
AGGATTO	110 EGGGACCCTGO	120 CGCGGAACAT	130 GGAGAACATC	140 ACATCAGGAT	150 TCCT
AGGACCO	160 CCTTCTCGTG1	170 TTACAGGCGG	180 GGTTTTTCTT	190 GTTGACAAGA	200 ATCC
	210	220	230	240	250
TCACAAT	PACCGCAGAGI				
	260	270	280	290	300
GGGGGAA	ACTACCGTGT	STCTTGGCCA	AAATTCGCAG'	TCCCCAACCT	CCAA
	310	320	330	340	350
TCACTCA	CCAACCTCCI	TGTCCTCCAA	CTTGTCCTGG'	TTATCGCTGG	ATGT
	360	370			400
GTCTGC	GCGTTTTATO	CATCTTCCTC	TTCATCCTGC'	TGCTATGCCT	CATC
	410	420	430		450
TTCTTGT	TGGTTCTTCT	rggactateri	AGGTATGTTG	CCCGTTTGTC	CTCT
	460	470		490	500
AATTCCA	AGGATCCTCAA	ACCACCAGCA	CGGGACCATG	CCGAACCTGC	ATGA
CM A CM CC		520			550
CIACIGO	CTCAAGGAACC	TCTATGTAT	CCTCCTGTT	GCTGTACCAA	ACCT
ACCCACC	560 GAAATTGCAC	570 ************************************	580 - מעררר מערמי		600
AOGGACC				1001999011	1000
ΑΑΑΑΤΤΟ	610 CTATGGGAGT	620 regecercae		640 CTGGCTCAGT	650 TTAC
TAGTGCC	660 CATTTGTTCAG	670 STGGTTCGTA	680 GGCTTTCCC	690 CCACTGTTTG	700 GCTT
TCAGTTA	710 ATATGGATGAT	720 GTGGTATTG	730 GGGGCCAAGT	740 CTGYACAGCA'	750 CTT
	760	770	780	790	800
GAGTCCC	TTTTTACCGC				
	810	820	830	840	850
TTTAAAC	CCTAACAAA				
	860	870	880	890	900
GTTATGT	CATTGGAAGI				
	010				

910 AAAATCAAAGAA

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LSPNSARSPCWWLQFRNSKPCSDYCLSLIVNLLEDWGPCAEHGEHHIRIP ${\tt RTPSRVTGGVFLVDKNPHNTAESRLVVDFSQFSRGNYRVSWPKFAVPNLQ}$ SLTNLLSSNLSWLSLDVSAAFYHLPLHPAAMPHLLVGSSGLSRYVARLSS NSRILNHQHGTMPNLHDYCSRNLYVSLLLLYQTYGRKLHLYSHPIILGFR KIPMGVGLSPFLLAQFTSAICSVVRRAFPHCLAFSYMDDVVLGAKSXQHL ESLFTAVTNFLLSLGIHLNPNKTKRWGYSLNFMGYVIGSYGSLPQEHIIQ KIKE

Figure 44

FHQTLQDPPAGG\$SSGTVNPVPTTASPLSSIFSRIGDPARNMENITSGFL GPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGTTVCLGQNSQSPTSN HSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYXGMLPVCPL IPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPTDGNCTCIPIPSSWAFG KFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLXSIL SPFLPR*PIFFCLWVYI*

Figure 45